Amendments to the Specification

Please amend the specification as follows:

Please amend paragraph [0052] as follows:

[0052] **Figure 7** presents results obtained when horse cytochrome c was quenched with or without 0.5M GuHCl, and then fragmented with either pepsin (P1), Newlase (P2) or Fungal Protease XIII (P3) coupled to perfusive supports (20 - 30 mg/ml). Considerable variation in digestion pattern and yield is seen with the varying conditions. The arrows at the top of the figure indicates the positions of the C- and N-termini of the aggregate peptides produced, highlighting the extreme degree of overlap of the set of peptide fragments produced **(SEQ ID NO: 1)**.

Please amend paragraph [0053] as follows:

[0053] **Figure 8** presents the fragmentation map obtained for a human von Willebrand Factor construct (denatured in 0.5 M GuHCl) employing a 40 second digestion on a pepsin column. In this study it was necessary to simultaneously reduce an internal disulfide bond by mixing TCEP (1.0 M final concentration) with the denaturant **(SEQ ID NO: 2)**.

Please amend paragraph [0054] as follows:

[0054] **Figure 9** presents the results of a deconvolution of fragmentation data obtained from chicken brain spectrin analyzed by high resolution hydrogen exchange. The deuterium content of the 113 useful peptides resulting from such fragmentation was determined from the raw mass spectroscopy data. Plots of deuterium buildup versus time were constructed for each peptide, and the number of amides exchanging in arbitrary "fast, medium and slow" classes

(light, medium, and dark grey colors respectively in the figure) determined for each peptide. An initial map of rates versus amino acid sequence was then constructed from this information, employing a strategy in which "pieces" (fragments) with uniform rate class (color), were first placed in register, and subsequent placement of more complexly colored pieces (two color then three color), and performed in a manner that required that the several "colors" in these peptides be reconciled vertically to conform with color placement of the preceding pieces. The average color (rate class) at each amide position was then determined and used to construct the initial map. Unmeasurable amide hydrogens (approximately 10% of the total amides in the 113 fragments, unmeasured either because of errors incurred because of the approximate (average) back-exchange calculation method employed, or because the very slowest exchanging amides were not measured in this experiment) were then fit to the provisional map in a manner that minimized deviation from said map, and a final map constructed by averaging this final placement of "pieces" **(SEQ ID NOs: 3 and 4)**.

Please amend paragraph [0057] as follows:

[0057] **Figure 12** illustrates the fragmentation map of RIIβ **(SEQ ID NO: 5)**.

Please amend paragraph [0059] as follows:

[0059] **Figure 14** collectively shows amide exchange of the dimerization/docking domain. Figure 14A shows percent deuteration for residues 2-19 **(SEQ ID NO: 6)**. The top bar for each ligand state represents t=10 s and the bottom bar represents t=3000 s. Secondary structure assignments are labeled above the sequence. Figure 14B plots the number of deuterons incorporated as a function of time for residues 15-19 in cAMP-free (●), cAMP-bound (■), and C-subunit bound (▲) conformations of RIIβ.

Please amend paragraph [0060] as follows:

[0060] **Figure 15** collectively shows amide exchange of the linker region. Figure 15A shows percent deuteration for residues 28-130 **(SEQ ID NO: 7)**. The top bar for each ligand state represents t=10 s and the bottom bar represents t=3000 s. Secondary structure assignments are labeled above the sequence. Figure 15 plots the number of deuterons incorporated as a function of time for residues 102-115 in cAMP-free (●), cAMP-bound (■), and C-subunit bound (▲) conformations of RIIβ.

Please amend paragraph [0061] as follows:

[0061] **Figure 16** collectively shows amide exchange of PBCs. Figure 16A is a ribbon diagram of cAMP-binding domains highlighting residues 222-224 (cA:αP), 228-233 (cA:PBC), 341-353 (cB:β6/αP), and 354-363 (cB:PBC) **(SEQ ID NOs: 8 and 9)**. Figure 16B shows percent deuteration for residues of cAMP-binding pockets. The top bar for each ligand state represents t=10 s and the bottom bar represents t=3000 s. Secondary structure assignments are labeled above the sequence. Figure 16C plots the number of deuterons incorporated as a function of time for sample residues 228-233 in cAMP-free (●), cAMP-bound (■), and C-subunit bound (▲) conformations of RIIβ. This plot is representative of all 4 peptides.

Please amend paragraph [0062] as follows:

[0062] **Figure 17** collectively shows amide exchange of cAMP-binding domain peptides showing increased deuteration upon C-subunit binding. Figure 17A is a ribbon diagram of the cB domain highlighting residues 303-312 (cB:β3) 321-325 (cB:β4), 377-379 (cB:αB) 390-396 (cB:αC), and 399-401 (cB:αC). Figure 17B shows percent deuteration for each ligand state at

t=10 s (top bar) and t=3000 s (bottom bar) **(SEQ ID NOs: 10-12, respectively in order of appearance)**. Secondary structure assignments are labeled above the sequence. Figure 17C plots the number of deuterons incorporated as a function of time in cAMP-free (●), cAMP-bound (■), and C-subunit bound (▲) conformations of RIIβ for residues 390-396 and 399-401. The plot for residues 390-396 is representative of the remaining 3 peptides.

Please amend paragraph [0063] as follows:

[0063] **Figure 18** collectively shows amide exchange for cAMP-binding domain peptides showing decreased deuteration upon C-subunit binding. Figure 18A is a ribbon diagram of cAMP-binding domains highlighting residues 150-152 ($\alpha X_n'$), 253-268 (cA:αC,αC'), 271-277 (cA:αC"), 278-281 (cB:αA), and 381-387 (cB:αB/αC). Figure 18B shows percent deuteration for each ligand state at t=10 s (top bar) and t=3000 s (bottom bar) **(SEQ ID NOs: 13-15, respectively in order of appearance)**. Secondary structure assignments are labeled above the sequence. Figure 18C plots the number of deuterons incorporated as a function of time for cAMP-free (●), cAMP-bound (■), and C-subunit bound (▲) conformations of RIIβ.

Please amend paragraph [0065] as follows:

[0065] **Figure 20** illustrates the exchange map of TM0160 parent protein as compared to a daughter construct containing a C-terminal deletion of the disordered region **(SEQ ID NOs: 16 and 17)**.